AMENDMENTS TO THE CLAIMS

1. (Currently amended) A method for whole genome amplification comprising:

(a) treating genomic DNA with a ~~modifying agent selected from the group consisting of~~ bisulphite~~, acetate and citrate which modifies~~ reagent to form treated genomic DNA, removing the bisulphite reagent and incubating the treated genomic DNA at pH of between 10 and less than 12.5 to form substantially unfragmented single stranded modified DNA, wherein cytosine bases ~~but does not modify 5'-methyl-cytosine bases under conditions to form single stranded modified DNA, wherein the treatment does not result in substantial DNA fragmentation~~ but not 5'-methyl-cytosine bases in the genomic DNA are modified to uracil bases to form the modified DNA;

(b) providing a population of random X-mers of exonuclease-resistant primers capable of binding to at least one strand of the modified DNA, wherein X is an integer 3 or greater, and wherein the primers are formed of two populations of primers, the first population comprising random X-mers containing only the bases A, G and T, and the second population comprising random X-mers containing only the bases A, C and T;

(c) contacting the modified DNA and the population of random X-mers with nucleotides and a polymerase capable of amplifying double stranded DNA; and

(d) allowing the polymerase to amplify the modified DNA.

2. (Canceled)

3. (Canceled)

4. (Currently amended) The method according to claim 1 wherein the ~~agent~~ bisulphite reagent is sodium bisulphite.

5. (Previously presented) The method according to claim 1 wherein the exonuclease-resistant primers are oligonucleotides or oligonucleotide analogues containing at least one intercalator pseudonucleotide forming an intercalating nucleic acid (INA).

6. (Original) The method according to claim 5 wherein the oligonucleotide or oligonucleotide analogue is selected from the group consisting of subunits of DNA, RNA, peptide nucleic acid (PNA), hexitol nucleic acid (HNA), MNA, altritol nucleic acid (ANA), locked nucleic acid (LNA), cyclohexanyl nucleic acid (CAN), CeNA, TNA, (2'-NH)-TNA, nucleic acid based conjugates, (3'-NH)-TNA, α-L-Ribo-LNA, α-L-Xylo-LNA, β-D-Xylo-LNA, α-D-Ribo-LNA, [3.2.1]-LNA, Bicyclo-DNA, 6-Amino-Bicyclo-DNA, 5-epi-Bicyclo-DNA, α-Bicyclo-DNA, Tricyclo-DNA, Bicyclo[4.3.0]-DNA, Bicyclo[3.2.1]-DNA, Bicyclo[4.3.0]amide-DNA, β-D-Ribopyranosyl-NA, α-L-Lyxopyranosyl-NA, 2'-R-RNA, 2'-OR-RNA, α-L-RNA, and β-D-RNA.

7. (Previously presented) The method according to claim 1 wherein the exonuclease-resistant primers are intercalating nucleic acids (INAs) formed from oligonucleotides.

8. (Previously presented) The method according to claim 1 wherein the primers are formed of two populations of INA primers, the first population being random X-mers containing only the bases A, G and T, and the second population comprising random X-mers containing only the bases A, C and T.

9. (Original) The method according to claim 8 wherein one population of primers is capable of binding to one strand of DNA while the other population of primers is capable of binding to a complimentary synthesized strand of the DNA stand to which the first population of primers bind.

10. (Original) The method according to claim 9 wherein the primers contain from 3 to 40 bases.

11. (Original) The method according to claim 10 wherein the primers contain about 6 to 20 bases.

12. (Previously presented) The method according to claim 1 wherein the polymerase is phi29, a modified version thereof, or a functional equivalent thereof capable of amplifying double stranded DNA *in vitro* without the need to denature the DNA.

13. (Original) The method according to claim 12 wherein the polymerase is phi29.

14. (Previously presented) The method according to claim 1 wherein the polymerase comprises a polymerase cocktail comprising a mixture of at least one proof-reading DNA polymerase and at least one non proof-reading DNA polymerase, wherein the ratio of proof-reading polymerase to non proof-reading polymerase is at least about 1:2.

15. (Original) The method according to claim 14 wherein the proof-reading DNA polymerase is selected from the group consisting of Pfu polymerase, Pfu polymerase turbo, Vent polymerase, Vent exo- polymerase, Pwo polymerase, $9^{o}N_{m}$DNA polymerase, Therminator, *Pfx* DNA polymerase, Expand DNA polymerase, rTth DNA polymerase, and DyNAzyme EXT Polymerase.

16. (Previously presented) The method according to claim 14 wherein the non proof-reading DNA polymerase is selected from the group consisting of Taq polymerase, Taq polymerase Stoffel fragment, Advantage DNA polymerase, AmpliTaq, Amplitaq Gold, Titanium Taq polymerase, KlenTaq DNA polymerase, Platinum Taq polymerase, and Accuprime Taq polymerase.

17. (Previously presented) The method according to claim 14 wherein the ratio of proof-reading polymerase to non-proof-reading polymerase is at least about 1:5.

18. (Original) The method according to claim 17, wherein the ratio of proof-reading polymerase to non-proof-reading polymerase about 1:10.

19. (Previously presented) The method according to claim 14 wherein step (d) is carried out by DNA thermal cycling.

20. (Withdrawn) A population of random X-mers of exonuclease-resistant primers capable of binding to at least one strand of modified DNA in whole genome amplification, where X is an integer of 3 or greater, and wherein the primers are formed of two populations of primers, the first population being random X-mers containing the bases A, G and T, and the second population comprising random X-mers containing the bases A, C and T.

21. (Withdrawn) The population of primers according to claim 20 wherein the exonuclease-resistant primers are intercalating nucleic acids (INAs) formed from oligonucleotides.

22. (Withdrawn) The population of primers according to claim 21 wherein the random primers are formed of two populations of INA primers, the first population being random X-mers containing the bases A, G and T, and the second population comprising random X-mers containing the bases A, C and T.

23. (Withdrawn) The population of primers according to claim 22 wherein one population of primers is capable of binding to one strand of DNA while the other population of primers is capable of binding to a complimentary synthesized strand of the DNA stand to which the first population of primers bind.

24. (Withdrawn) The population of primers according to claim 23 wherein the primers contain from 3 to 40 bases.

25. (Withdrawn) The population of primers according to claim 24 wherein the primers contain about 6 to 20 bases.

26. (Withdrawn) A kit containing a population of primers according to claim 20 for use in whole genome amplification.

27. (Withdrawn) Use of a population of primers according to claim 20 for whole genome amplification.

28. (Withdrawn) A kit containing a population of primers according to claim 20, and a polymerase capable of amplifying double stranded DNA for use in whole genome amplification.

29. (Withdrawn) The kit according to claim 28 wherein the polymerase is selected from the group consisting of phi29, a modified version thereof, a functional equivalent thereof capable of amplifying double stranded DNA *in vitro* without the need to denature the DNA and a

polymerase cocktail comprising a mixture of at least one proof-reading DNA polymerase and at least one non proof-reading DNA polymerase.

30. (Previously presented) The method according to claim 1 wherein cytosine methylation of the genomic DNA is determined from the amplified DNA.

31. (New) The method according to claim 1 wherein the bisulphite reagent is sodium metabisulphite.

32. (New) The method according to claim 1 wherein the treated genomic DNA is incubated at about 37°C to about 96°C.

33. (New) The method according to claim 1 wherein the treated genomic DNA is incubated for 2 minutes to 96 hours.

34. (New) The method according to claim 1 wherein the treated genomic DNA is incubated at pH 10.5.